

# SCORE Search Results Details for Application 10580141 and Search Result 20071214\_074747\_us-10-580-141-1.rng.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
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This page gives you Search Results detail for the Application 10580141 and Search Result 20071214\_074747\_us-10-580-141-1.rng.

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MM nucleic - nucleic search, using sw model

Run on: December 14, 2007, 18:27:30 ; Search time 405 Seconds  
(without alignments)  
44354.964 Million cell updates/sec

Title: US-10-580-141-1  
Perfect score: 1662  
Sequence: 1 atgcgaataggagatcctat.....cggagaatacacatatctat 1662

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_200711:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000:\*  
4: geneseqn2001a:\*  
5: geneseqn2001b:\*  
6: geneseqn2002a:\*  
7: geneseqn2002b:\*  
8: geneseqn2003a:\*  
9: geneseqn2003b:\*  
10: geneseqn2003c:\*  
11: geneseqn2003d:\*  
12: geneseqn2004a:\*  
13: geneseqn2004b:\*  
14: geneseqn2004c:\*  
15: geneseqn2004d:\*  
16: geneseqn2005a:\*

	42	40.2	2.4	37373	17	AEC76962	Aec76962 Bacillus
	43	40	2.4	48	2	AAZ28181	Aaz28181 Chlamydia
	44	40	2.4	48	3	AAZ99164	Aaz99164 Chlamydia
c	45	39.8	2.4	2000	8	ADA71938	Ada71938 Rice gene

# ALIGNMENTS

## RESULT 1

AD32410

ID AAD32410 standard; DNA; 1662 BP.

IX

XC AAD32410;

IX

DT 18-JUN-2002 (first entry)

IX

DE Chlamydia trachomatis MoPn omcB/ompB gene.

IX

W Chlamydiaceae family; chronic infection; persistent infection; pyk; nlpD;  
W Cpn0585; regulatory pathway; biosynthetic pathway; ompA; ompB; hsp60;  
W lipopolysaccharide; cardiovascular system; respiratory tract; therapy;  
W genital tract; reproductive system; atherosclerotic tissue; macrophage;  
W multiple sclerosis; conjunctiva; prophylaxis; antibacterial; gene; ds.

IX

DS Chlamydia trachomatis.

IX

TH Key Location/Qualifiers

TT CDS 1. .1662

TT /\*tag= a

TT /product= "Chlamydia trachomatis MoPn omcB/ompB protein"

TT /note= "CDS does not include stop codon"

TT /partial

IX

DN WO200214516-A1.

IX

DD 21-FEB-2002.

IX

DF 17-AUG-2001; 2001WO-AU001021.

IX

DR 18-AUG-2000; 2000AU-00009540.

IX

DA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

DA (MATH/) MATHEWS S A.

IX

DI Timms P;

IX

DR WPI; 2002-269197/31.

DR P-PSDB; AAE32410.

IX

DT Detecting Chlamydial organism in its persistent phase by detecting  
DT expression change of range of genes belonging to their respective  
DT biosynthetic pathways when expression is compared to that of organism in  
DT lytic phase.

IX

DS Disclosure; Page 156-159; 196pp; English.

IX



yb 421 GTAATCATTACACAGCAATTACCATGCGAAGCAGAGTTTGTAGCAGTGATCCAGCTACT 480  
 y 481 ACTCCTACTGCTGATGGTAAGCTAGTTTGGAAAATTGATCGGTTAGGACAGGGCGAAAAG 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 481 ACTCCTACTGCTGATGGTAAGCTAGTTTGGAAAATTGATCGGTTAGGACAGGGCGAAAAG 540  
 y 541 AGTAAATTACTGTATGGGTAAAACCTCTTAAAGAAGGTTGCTGCTTTACAGCTGCAACG 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 541 AGTAAATTACTGTATGGGTAAAACCTCTTAAAGAAGGTTGCTGCTTTACAGCTGCAACG 600  
 y 601 GTTTGTGCTTGTCAGAGATCCGTTTCGGTTACGAAATGTGGCCAGCCTGCTATCTGTGTT 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 601 GTTTGTGCTTGTCAGAGATCCGTTTCGGTTACGAAATGTGGCCAGCCTGCTATCTGTGTT 660  
 y 661 AAACAGGAAGGTCCAGAAAGCGCATGTTTGCGTTGCCAGTAACTTATAGAATTAATGTA 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 661 AAACAGGAAGGTCCAGAAAGCGCATGTTTGCGTTGCCAGTAACTTATAGAATTAATGTA 720  
 y 721 GTCAACCAAGGAACAGCAACAGCACGTAATGTTGTTGTGGAAAATCCTGTTCCAGATGGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 721 GTCAACCAAGGAACAGCAACAGCACGTAATGTTGTTGTGGAAAATCCTGTTCCAGATGGC 780  
 y 781 TATGCTCATGCATCCGGACAGCGTGTATTGACATATACTCTTGGGGATATGCAACCTGGA 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 781 TATGCTCATGCATCCGGACAGCGTGTATTGACATATACTCTTGGGGATATGCAACCTGGA 840  
 y 841 GAACAGAGAACAATCACCGTGGAGTTTGTCCGCTTAAACGTGGTCGAGTCACAAATATT 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 841 GAACAGAGAACAATCACCGTGGAGTTTGTCCGCTTAAACGTGGTCGAGTCACAAATATT 900  
 y 901 GCTACAGTTTCTTACTGTGGTGGACACAAAATACTGCTAGCGTAACAACAGTGATCAAT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 901 GCTACAGTTTCTTACTGTGGTGGACACAAAATACTGCTAGCGTAACAACAGTGATCAAT 960  
 y 961 GAGCCTTGCGTGCAAGTTAACATCGAGGGAGCAGATTGGTCTTATGTTTGTAAGCCTGTA 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 961 GAGCCTTGCGTGCAAGTTAACATCGAGGGAGCAGATTGGTCTTATGTTTGTAAGCCTGTA 1020  
 y 1021 GAATATGTTATCTCTGTTTCTAACCCTGGTGACTTAGTTTTACGAGACGTTGTAATTGAA 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 1021 GAATATGTTATCTCTGTTTCTAACCCTGGTGACTTAGTTTTACGAGACGTTGTAATTGAA 1080  
 y 1081 GATACGCTTCTCCTGGAATAACTGTTGTTGAAGCAGCTGGAGCTCAGATTTCTTGTAAT 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 1081 GATACGCTTCTCCTGGAATAACTGTTGTTGAAGCAGCTGGAGCTCAGATTTCTTGTAAT 1140  
 y 1141 AAATTGGTTTGGACTTTGAAGGAACTCAATCCTGGAGAGTCTTTACAATATAAGGTTCTA 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 1141 AAATTGGTTTGGACTTTGAAGGAACTCAATCCTGGAGAGTCTTTACAATATAAGGTTCTA 1200  
 y 1201 GTAAGAGCTCAAACCTCCAGGGCAATTCACAAACAACGTTGTTGTGAAAAGTTGCTCTGAT 1260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 1201 GTAAGAGCTCAAACCTCCAGGGCAATTCACAAACAACGTTGTTGTGAAAAGTTGCTCTGAT 1260  
 y 1261 TGCGGTATTTGTACTTCTTGCGCAGAAGCAACAACCTTACTGGAAAGGAGTTGCTGCTACT 1320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 yb 1261 TGCGGTATTTGTACTTCTTGCGCAGAAGCAACAACCTTACTGGAAAGGAGTTGCTGCTACT 1320

```

iy      1321 CATATGTGCGTAGTAGATACTTGTGATCCTATTTGCGTAGGAGAGAACTGTTTATCGT 1380
          |||
ob      1321 CATATGTGCGTAGTAGATACTTGTGATCCTATTTGCGTAGGAGAGAACTGTTTATCGT 1380

iy      1381 ATCTGTGTGACAAACAGAGGTTCTGCTGAAGATACAAATGTGTCCTTAATTTTGAAATTC 1440
          |||
ob      1381 ATCTGTGTGACAAACAGAGGTTCTGCTGAAGATACAAATGTGTCCTTAATTTTGAAATTC 1440

iy      1441 TCTAAAGAATTACAACCTATATCTTTCTCTGGACCAACTAAAGGAACCATTACAGGAAAC 1500
          |||
ob      1441 TCTAAAGAATTACAACCTATATCTTTCTCTGGACCAACTAAAGGAACCATTACAGGAAAC 1500

iy      1501 ACGGTAGTGTTTGATTTCGTTACCTAGATTAGGTTCTAAAGAACTGTAGAGTTTCTGTA 1560
          |||
ob      1501 ACGGTAGTGTTTGATTTCGTTACCTAGATTAGGTTCTAAAGAACTGTAGAGTTTCTGTA 1560

iy      1561 ACGTTGAAAGCAGTATCCGCTGGAGATGCTCGTGGGGAAGCTATTCTTTCTTCCGATACA 1620
          |||
ob      1561 ACGTTGAAAGCAGTATCCGCTGGAGATGCTCGTGGGGAAGCTATTCTTTCTTCCGATACA 1620

iy      1621 TTGACAGTTCCTGTATCTGATACGGAGAATACACATATCTAT 1662
          |||
ob      1621 TTGACAGTTCCTGTATCTGATACGGAGAATACACATATCTAT 1662

```

# RESULT 2

AEA49028

ID AEA49028 standard; DNA; 1662 BP.

IX

IC AEA49028;

IX

IT 11-AUG-2005 (first entry)

IX

IE Nucleotide sequence of 60KCRMP gene.

IX

IW 60KCRMP; cysteine-rich outer membrane protein; antibacterial; vaccine;

IW Chlamydia infection; gene; ds.

IX

IS Chlamydia muridarum.

IX

IH Key Location/Qualifiers

IT CDS 1. .1662

IT /\*tag= b

IT /product= "60KCRMP"

IT sig\_peptide 1. .111

IT /\*tag= a

IX

IN WO2005049837-A1.

IX

ID 02-JUN-2005.

IX

IF 22-NOV-2004; 2004WO-CA002004.

IX

IR 20-NOV-2003; 2003US-0481676P.

IX

IA (AVET ) AVENTIS PASTEUR LTD.

# SCORE Search Results Details for Application 10580141 and Search Result 20071214\_075047\_us-10-580-141-2.rag.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

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DM protein - protein search, using sw model

Run on: December 14, 2007, 10:25:01 ; Search time 153 Seconds  
(without alignments)  
2174.075 Million cell updates/sec

Title: US-10-580-141-2  
Perfect score: 2882  
Sequence: 1 MRIGDPMNKLIRRAVTIFAV.....ILSSDTLTVPVSDTENTHIY 554

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200711:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000:\*  
4: geneseqp2001:\*  
5: geneseqp2002:\*  
6: geneseqp2003a:\*  
7: geneseqp2003b:\*  
8: geneseqp2004a:\*

36	138	4.8	688	4	ABB35307	Abb35307 Peptide #
37	138	4.8	688	4	AAM28810	Aam28810 Peptide #
38	138	4.8	688	4	ABG50180	Abg50180 Human liv
39	138	4.8	688	4	ABB20749	Abb20749 Protein #
40	138	4.8	688	4	AAM68511	Aam68511 Human bon
41	138	4.8	688	4	AAM16315	Aam16315 Peptide #
42	138	4.8	688	4	ABB30137	Abb30137 Peptide #
43	138	4.8	688	5	ABG38092	Abg38092 Human pep
44	138	4.8	1773	11	AEF06270	Aef06270 Human muc
45	137.5	4.8	1583	11	AES83364	Aes83364 S. agalac

## ALIGNMENTS

### RESULT 1

AAE20299

ID AAE20299 standard; protein; 554 AA.

XX

AC AAE20299;

XX

DT 15-JUN-2007 (revised)

DT 18-JUN-2002 (first entry)

XX

DE Chlamydia trachomatis MoPn omcB/ompB protein.

XX

KW Chlamydiaceae family; chronic infection; persistent infection; pyk; nlpD;  
 KW Cpn0585; regulatory pathway; biosynthetic pathway; ompA; ompB; hsp60;  
 KW lipopolysaccharide; cardiovascular system; respiratory tract; therapy;  
 KW genital tract; reproductive system; atherosclerotic tissue; macrophage;  
 KW multiple sclerosis; conjunctiva; prophylaxis; antibacterial; BOND\_PC;  
 KW 60 kDa outer membrane protein; OmcB;  
 KW 60 kDa outer membrane protein [Chlamydia muridarum Nigg].

XX

DS Chlamydia trachomatis.

XX

PN WO200214516-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2001; 2001WO-AU001021.

XX

PR 18-AUG-2000; 2000AU-00009540.

XX

PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

PA (MATH/) MATHEWS S A.

XX

PI Timms P;

XX

DR WPI; 2002-269197/31.  
DR N-PSDB; AAD32410.  
DR PC:NCBI; gi7190756.  
DR PC:SWISSPROT; Q9PJV0.

KX

PT Detecting Chlamydial organism in its persistent phase by detecting  
PT expression change of range of genes belonging to their respective  
PT biosynthetic pathways when expression is compared to that of organism in  
PT lytic phase.

KX

PS Disclosure; Page 159-161; 196pp; English.

KX

CC The invention relates to composition and methods for detecting organisms  
CC of the Chlamydiaceae family, including species of Chlamydophila and  
CC Chlamydia, in the persistent phase of their developmental cycle and for  
CC the diagnosis of chronic or persistent infections caused by such  
CC organisms. The composition is useful for modulating the expression of  
CC gene such as pyk, nlpD, Cpn0585, a gene belonging to same regulatory/  
CC biosynthetic pathway and ompA, ompB, hsp60, a gene involved in  
CC lipopolysaccharide biosynthesis. It is also useful for modulating the the  
CC level and/or functional activity of an expression product of these genes,  
CC where the gene is present in an epithelial cell (selected from  
CC cardiovascular system, respiratory tract, genital tract, reproductive  
CC system or conjunctiva), macrophage, or a cell associated with  
CC atherosclerotic tissue or associated with multiple sclerosis brain  
CC tissue. The composition is useful for treatment and/or prophylaxis of a  
CC chronic infection caused by an organism of the Chlamydiaceae family in a  
CC patient. Antigen associated with the persistent phase of the  
CC developmental cycle of an organism of the Chlamydiaceae family, is useful  
CC in the manufacture of a medicament, for treating and/or preventing  
CC Chlamydiaceae infection in a patient. The present sequence is Chlamydia  
CC trachomatis MoPn omcB/ompB protein

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed  
CC information from BOND.

KX

3Q Sequence 554 AA;

Query Match 100.0%; Score 2882; DB 5; Length 554;  
Best Local Similarity 100.0%; Pred. No. 1.3e-246;  
Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 MRIGDPMNKLIRRAVTIFAVTSVASLFASGVLETSMAESLSTNVISLADTKAKETTSHQK 60  
|||

2b 1 MRIGDPMNKLIRRAVTIFAVTSVASLFASGVLETSMAESLSTNVISLADTKAKETTSHQK 60

2y 61 DRKARKNHQNRTSVVRKEVTAVRDTKAVEPRQDSCFGKMYTVKVNDNRNVEIVQSVPEYA 120  
|||

2b 61 DRKARKNHQNRTSVVRKEVTAVRDTKAVEPRQDSCFGKMYTVKVNDNRNVEIVQSVPEYA 120



2y	121	TVGSPYPIEITAIGKRDCVDVIITQQLPCEAEFVSSDPATTPTADGKLVWKIDRLGQGEK	180
2b	121	TVGSPYPIEITAIGKRDCVDVIITQQLPCEAEFVSSDPATTPTADGKLVWKIDRLGQGEK	180
2y	181	SKITVWVKPLKEGCCFTAATVCACPEIRSVTKCGQPAICVKQEGPESACLRCPVTYRINV	240
2b	181	SKITVWVKPLKEGCCFTAATVCACPEIRSVTKCGQPAICVKQEGPESACLRCPVTYRINV	240
2y	241	VNQGTATARNVVVENPVPDGYAHASGQRVLTYYTLGDMQPGEQRTITVEFCPLKRGRVTNI	300
2b	241	VNQGTATARNVVVENPVPDGYAHASGQRVLTYYTLGDMQPGEQRTITVEFCPLKRGRVTNI	300
2y	301	ATVSYCGGHKNTASVTTVINEPCVQVNIEGADWSYVCKPVEYVISVSNPGDLVLRDVEIE	360
2b	301	ATVSYCGGHKNTASVTTVINEPCVQVNIEGADWSYVCKPVEYVISVSNPGDLVLRDVEIE	360
2y	361	DTLSPGITVVEAAGAQISCNKLVWTLKELNPGESLQYKVLVRAQTPGQFTNNVVVKSCSD	420
2b	361	DTLSPGITVVEAAGAQISCNKLVWTLKELNPGESLQYKVLVRAQTPGQFTNNVVVKSCSD	420
2y	421	CGICTSCAEATTYWKGVAAATHMCVVDTCDPICVGENTVYRICVTNRGSAEDTNVSLILKF	480
2b	421	CGICTSCAEATTYWKGVAAATHMCVVDTCDPICVGENTVYRICVTNRGSAEDTNVSLILKF	480
2y	481	SKELQPISFSGPTKGTITGNTVVFDLPLRLGSKETVEFSVTLKAVSAGDARGEAILSSDT	540
2b	481	SKELQPISFSGPTKGTITGNTVVFDLPLRLGSKETVEFSVTLKAVSAGDARGEAILSSDT	540
2y	541	LTVPVSDTENTHIY	554
2b	541	LTVPVSDTENTHIY	554

RESULT 2

AEA49029

ID AEA49029 standard; protein; 554 AA.

KX

AC AEA49029;

KX

DT 15-JUN-2007 (revised)

DT 11-AUG-2005 (first entry)

KX

DE Amino acid sequence of a 60KCRMP gene.

KX

KW 60KCRMP; cysteine-rich outer membrane protein; antibacterial; vaccine;

KW Chlamydia infection; BOND\_PC; 60 kDa outer membrane protein; OmcB;

KW 60 kDa outer membrane protein [Chlamydia muridarum Nigg].

KX